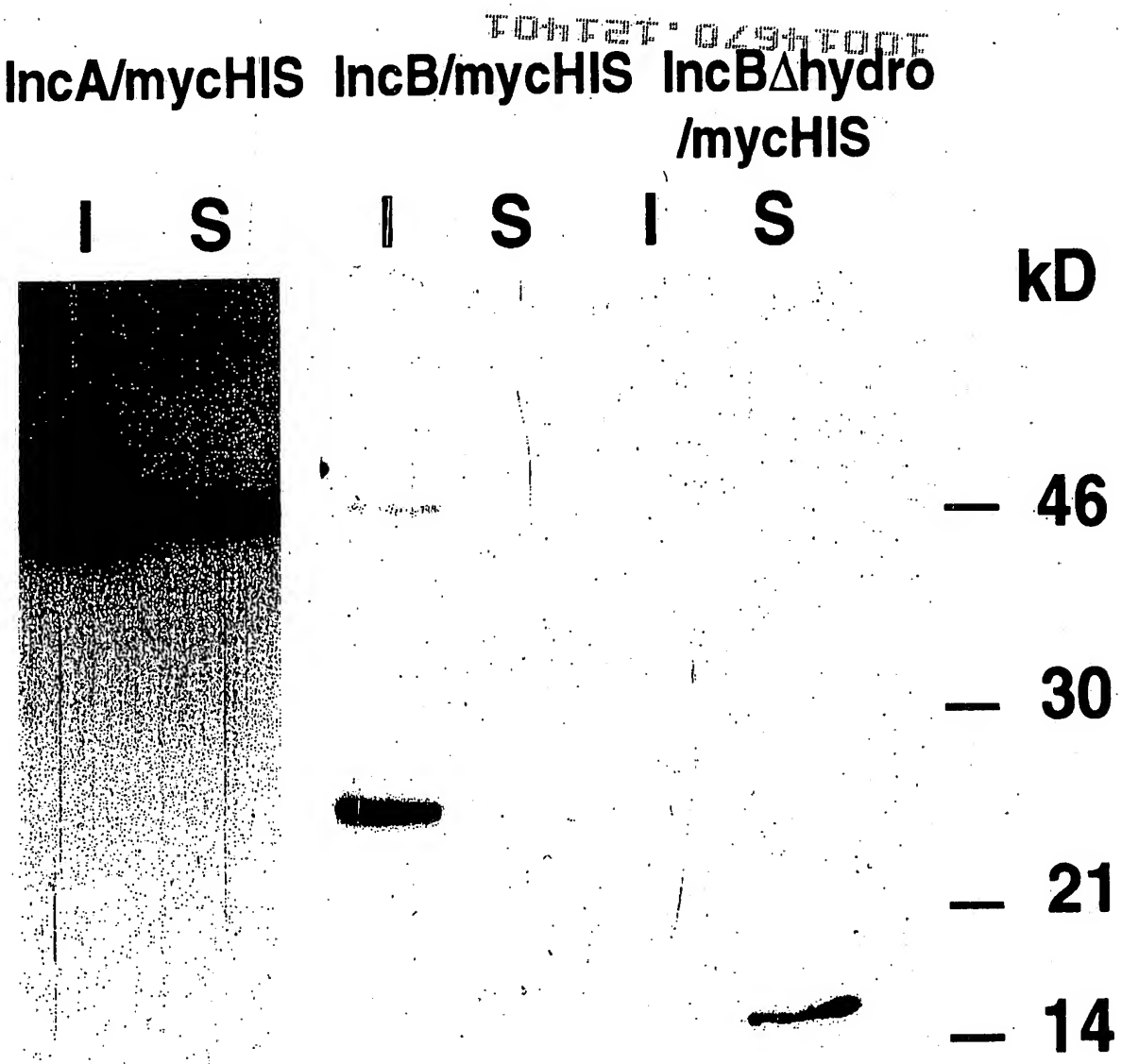

IncA/mycHIS
IncB/mycHIS
IncBΔhydro /mycHIS
I
S
I
S
I
S
kD
46
30
21
14

Figur 1

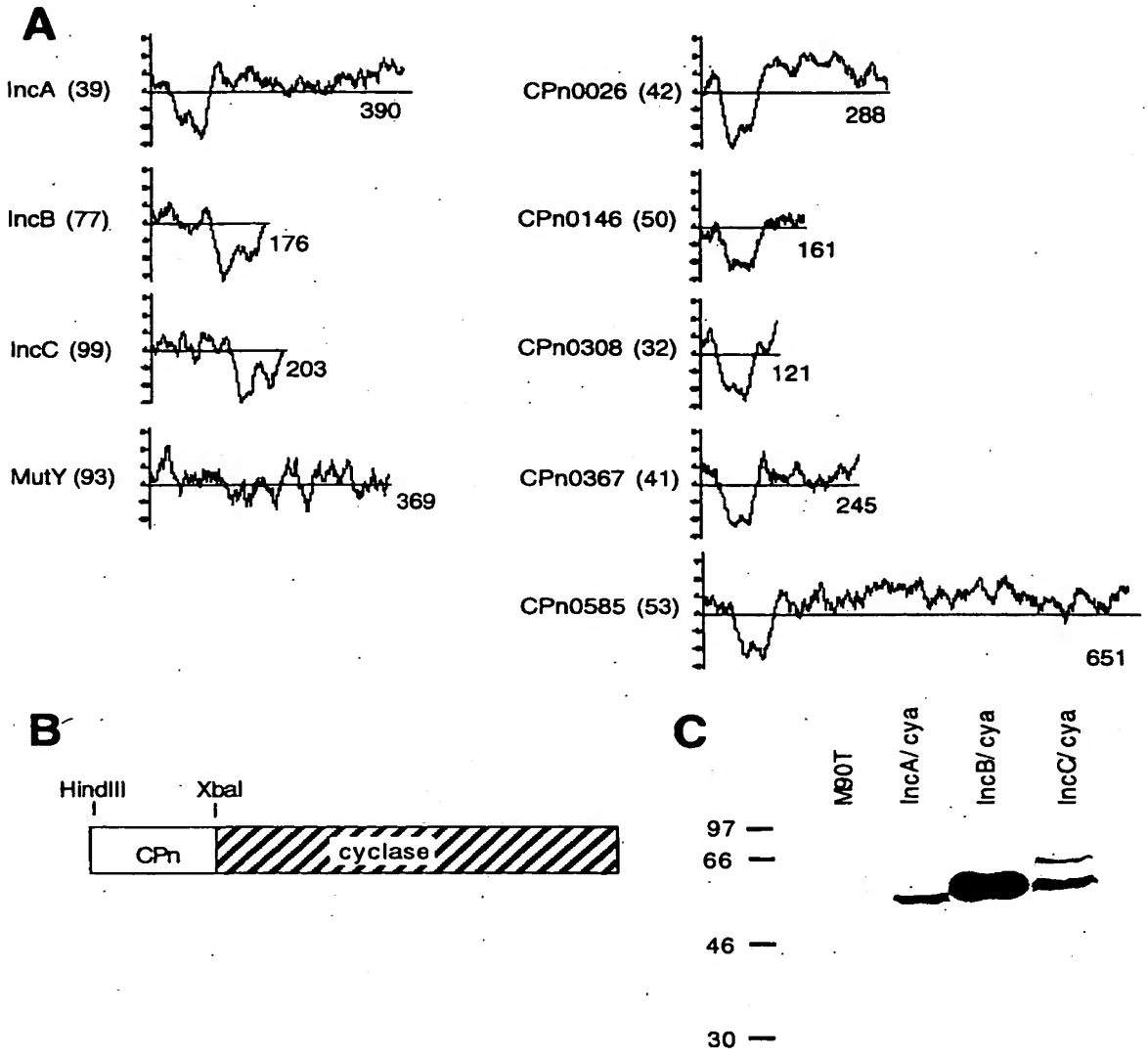
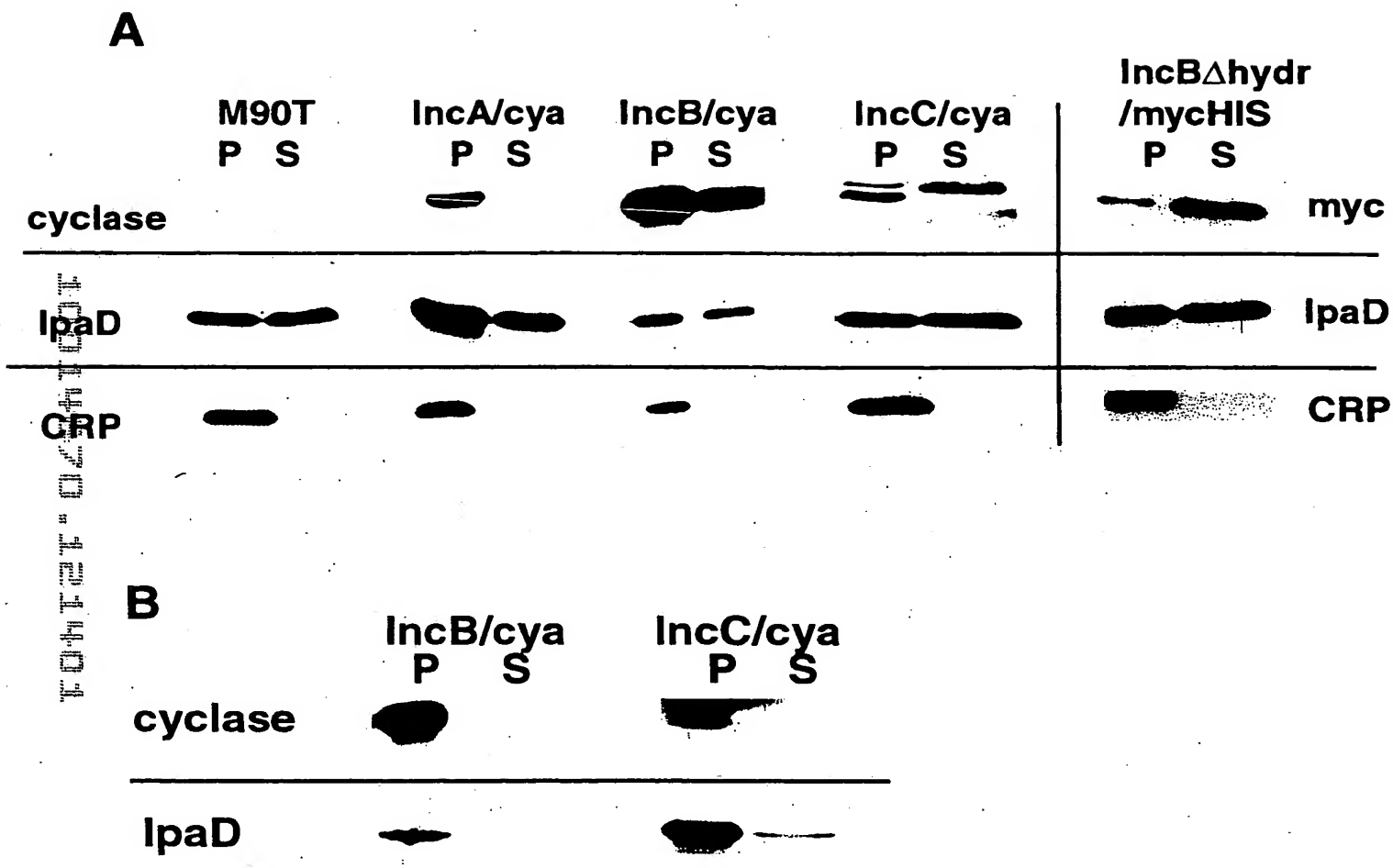

A
IncA (39)
390
IncB (77)
176
IncC (99)
203
MutY (93)
369
CPn0026 (42)
288
CPn0146 (50)
161
CPn0308 (32)
121
CPn0367 (41)
245
CPn0585 (53)
651
B
HindIII
XbaI
CPn
cyclase
C
M90T
IncA/ cya
IncB/ cya
IncC/ cya
97
66
46
30

Figure 2


A
M90T
P S
IncA/cya
P S
IncB/cya
P S
IncC/cya
P S
IncBΔhydr
/mycHIS
P S
cyclase
myc
IpaD
IpaD
CRP
CRP

B
IncB/cya
P S
IncC/cya
P S
cyclase
IpaD

Figure 3

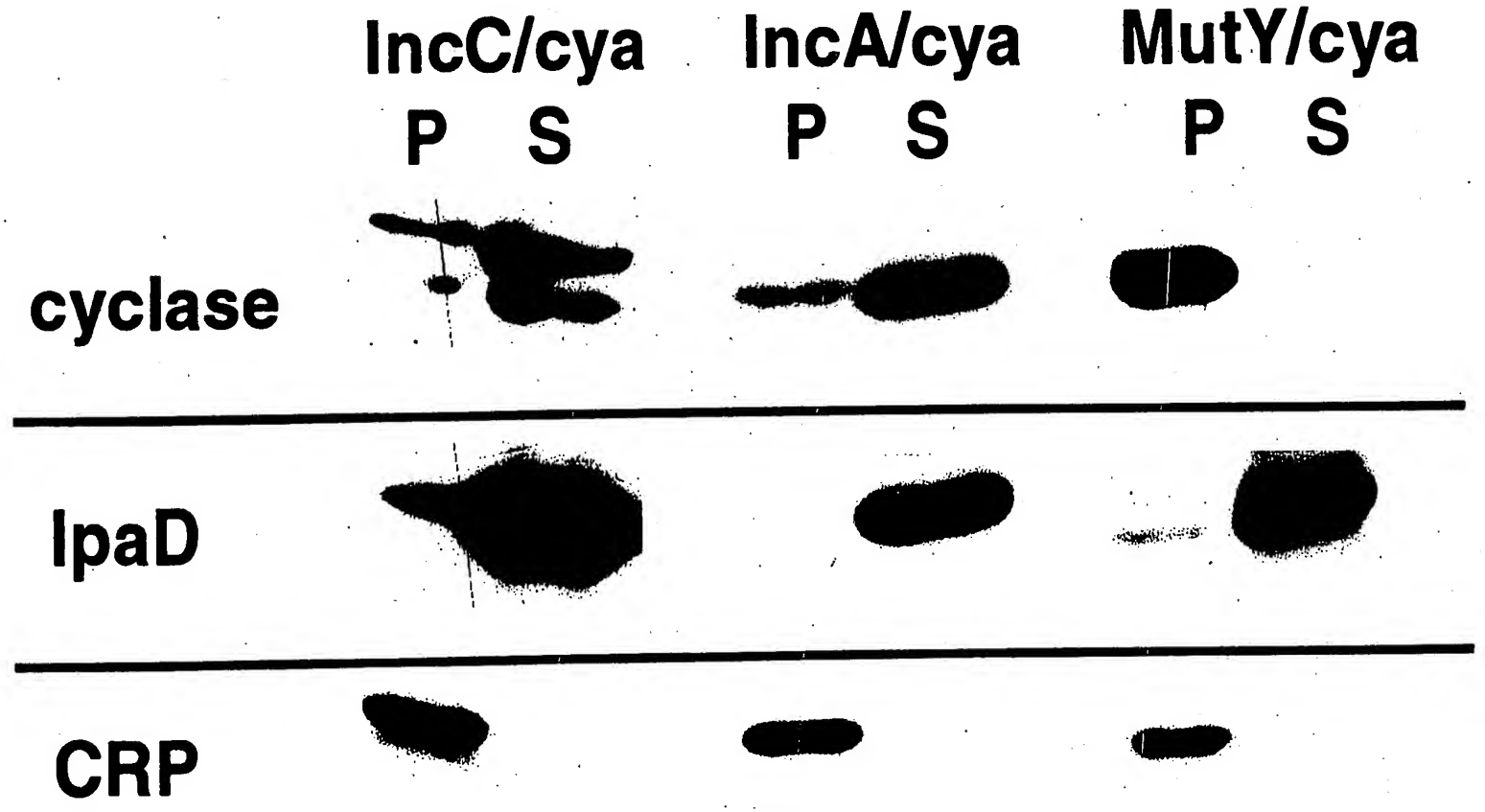


Figure 4

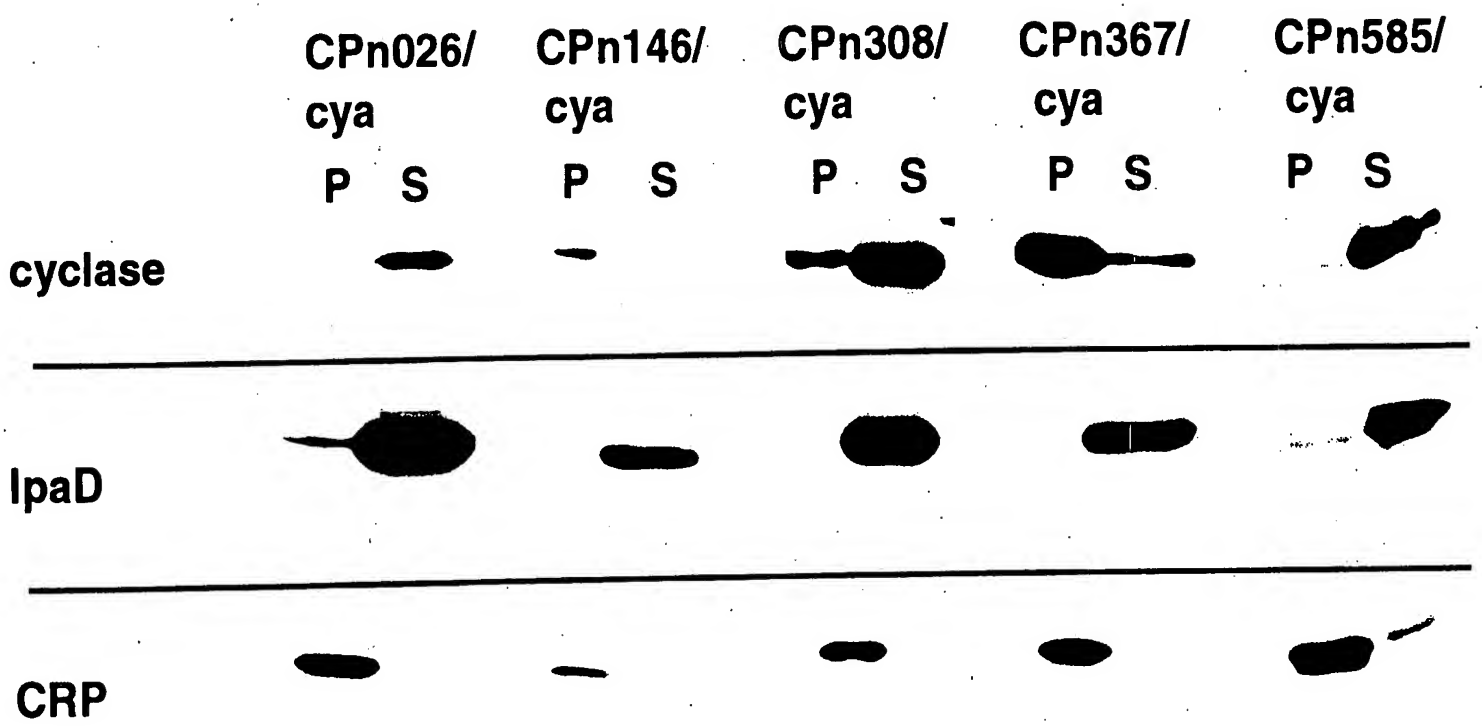

CPn026/ cya
CPn146/ cya
CPn308/ cya
CPn367/ cya
CPn585/ cya
P S
P S
P S
P S
P S
cyclase
IpaD
CRP

Figure 5

Figure 1: Full-length Sequence of *C. pneumoniae* 76kDa Gene.

```
ataaaatctt taaaaacagg ctcgcattaa ttattagtga gagcttttt tttatttttt 60

ataataaaac taaaagattt ttattatttt ttgagttttt atg gtt aat cct att   115
                                              Met Val Asn Pro Ile
                                                1               5

ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat ctt   163
Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp Leu
               10                  15                  20

tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa gct   211
Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu Ala
           25                  30                  35

caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc gat   259
Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr Asp
       40                  45                  50

tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc atg   307
Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu Met
   55                  60                  65

agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct tct   355
Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser Ser
70                  75                  80                  85

act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct acg   403
Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro Thr
               90                  95                 100

cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca gct   451
Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr Ala
           105                 110                 115

tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct gct   499
Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala Ala
       120                 125                 130

ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg gct   547
Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala Ala
   135                 140                 145

act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat gcc   595
Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn Ala
150                 155                 160                 165

gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat gct   643
Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr Ala
               170                 175                 180

tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc ttc   691
Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser Phe
           185                 190                 195
```

Figure 1 (continued)

```
gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac aaa   739
Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn Lys
        200                 205                 210

gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca ggg   787
Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro Gly
    215                 220                 225

aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct aca   835
Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala Thr
230                 235                 240                 245

gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat ttt   883
Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr Phe
                250                 255                 260

gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat aac   931
Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn Asn
            265                 270                 275

agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct aag   979
Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala Lys
        280                 285                 290

aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att ctt  1027
Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile Leu
    295                 300                 305

caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa aat  1075
Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys Asn
310                 315                 320                 325

atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca gtt  1123
Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr Val
                330                 335                 340

gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt tcc  1171
Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val Ser
            345                 350                 355

atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg tct  1219
Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met Ser
        360                 365                 370

ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat tct  1267
Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp Ser
    375                 380                 385

caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa gcc  1315
Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys Ala
390                 395                 400                 405

gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa gct  1363
Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys Ala
                410                 415                 420
```

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Figure 1 (continu d)

```
tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc aat   1411
Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu Asn
          425                 430                 435

gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gtt cct   1459
Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val Pro
      440                 445                 450

ccc gct gca gca agt tct ata ggg tca tct gta aaa cag ctt tac aag   1507
Pro Ala Ala Ala Ser Ser Ile Gly Ser Ser Val Lys Gln Leu Tyr Lys
  455                 460                 465

acc tca aaa tct aca ggt tct gat tat aaa aca cag ata tca gca ggt   1555
Thr Ser Lys Ser Thr Gly Ser Asp Tyr Lys Thr Gln Ile Ser Ala Gly
470                 475                 480                 485

tat gat gct tac aaa tcc atc aat gat gcc tat ggt agg gca cga aat   1603
Tyr Asp Ala Tyr Lys Ser Ile Asn Asp Ala Tyr Gly Arg Ala Arg Asn
                490                 495                 500

gat gcg act cgt gat gtg ata aac aat gta agt acc ccc gct ctc aca   1651
Asp Ala Thr Arg Asp Val Ile Asn Asn Val Ser Thr Pro Ala Leu Thr
          505                 510                 515

cga tcc gtt cct aga gca cga aca gaa gct cga gga cca gaa aaa aca   1699
Arg Ser Val Pro Arg Ala Arg Thr Glu Ala Arg Gly Pro Glu Lys Thr
      520                 525                 530

gat caa gcc ctc gct agg gtg att tct ggc aat agc aga act ctt gga   1747
Asp Gln Ala Leu Ala Arg Val Ile Ser Gly Asn Ser Arg Thr Leu Gly
  535                 540                 545

gat gtc tat agt caa gtt tcg gca cta caa tct gta atg cag atc atc   1795
Asp Val Tyr Ser Gln Val Ser Ala Leu Gln Ser Val Met Gln Ile Ile
550                 555                 560                 565

cag tcg aat cct caa gcg aat aat gag gag atc aga caa aag ctt aca   1843
Gln Ser Asn Pro Gln Ala Asn Asn Glu Glu Ile Arg Gln Lys Leu Thr
                570                 575                 580

tcg gca gtg aca aag cct cca cag ttt ggc tat cct tat gtg caa ctt   1891
Ser Ala Val Thr Lys Pro Pro Gln Phe Gly Tyr Pro Tyr Val Gln Leu
          585                 590                 595

tct aat gac tct aca cag aag ttc ata gct aaa tta gaa agt ttg ttt   1939
Ser Asn Asp Ser Thr Gln Lys Phe Ile Ala Lys Leu Glu Ser Leu Phe
      600                 605                 610

gct gaa gga tct agg aca gca gct gaa ata aaa gca ctt tcc ttt gaa   1987
Ala Glu Gly Ser Arg Thr Ala Ala Glu Ile Lys Ala Leu Ser Phe Glu
  615                 620                 625

acg aac tcc ttg ttt att cag cag gtg ctg gtc aat atc ggc tct cta   2035
Thr Asn Ser Leu Phe Ile Gln Gln Val Leu Val Asn Ile Gly Ser Leu
630                 635                 640                 645
```

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Figure 1 (continued)

```
tat tct ggt tat ctc caa taacaacacc taagtgttcg tttggagaga          2083
Tyr Ser Gly Tyr Leu Gln
                650

ttattatgtg ctttggtaag gcctttgttg aggccttacc aacacactag aacgatcttc 2143

aataaataaa aga                                                    2156
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TOKTZT: 0459470T

Figure 2: Restriction enzyme map of *C. pneumoniae* 76kDa gene.

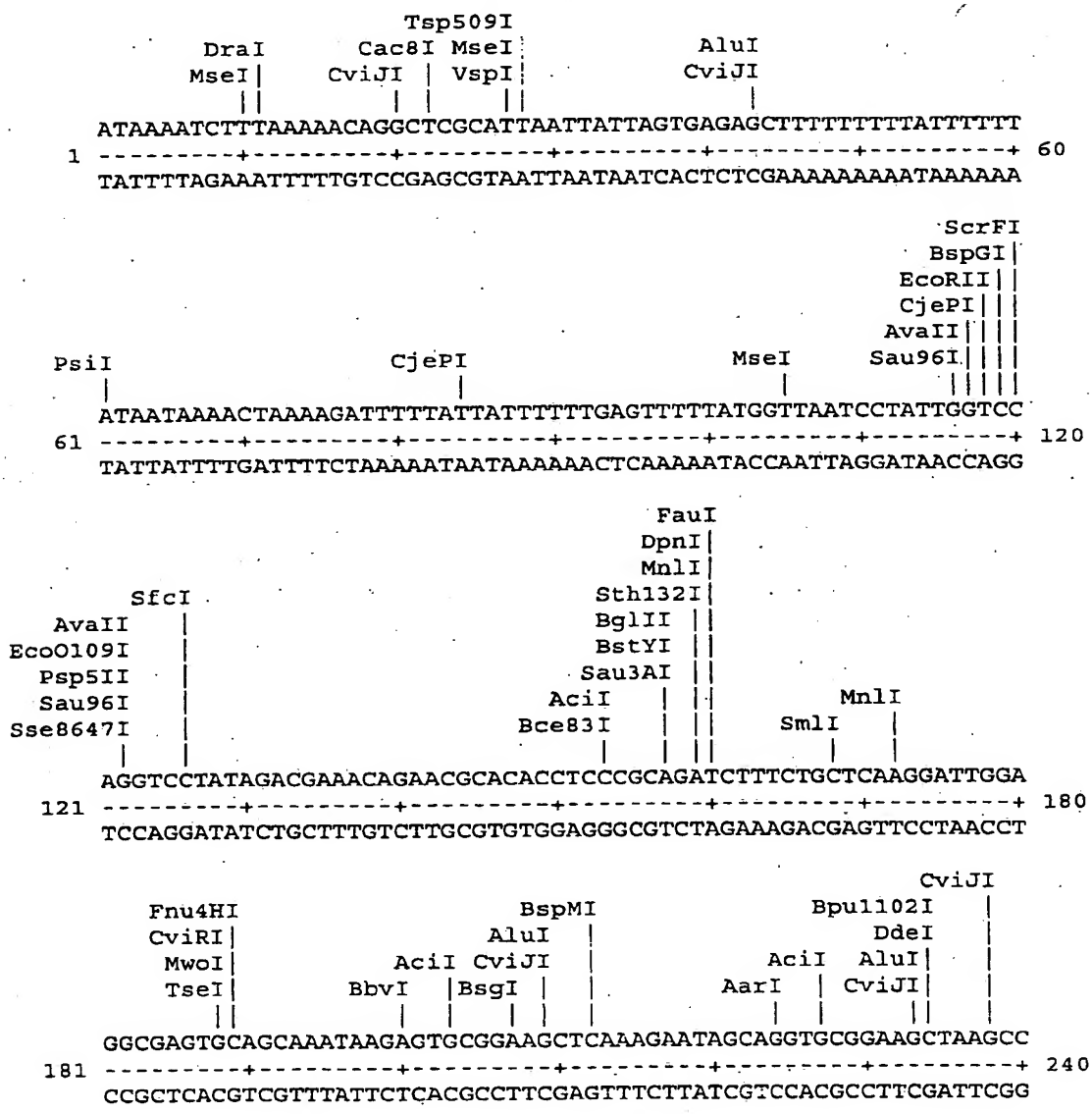
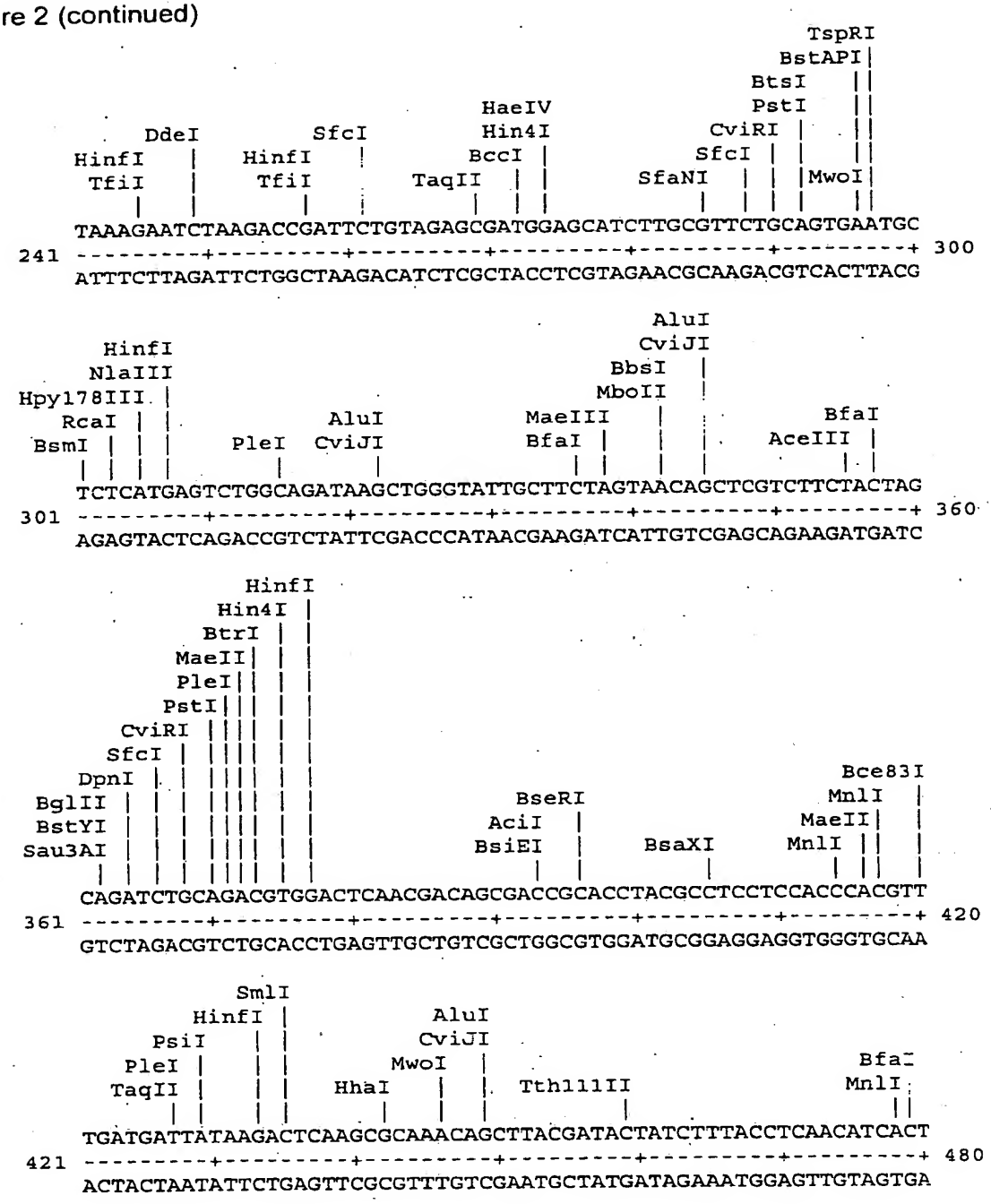
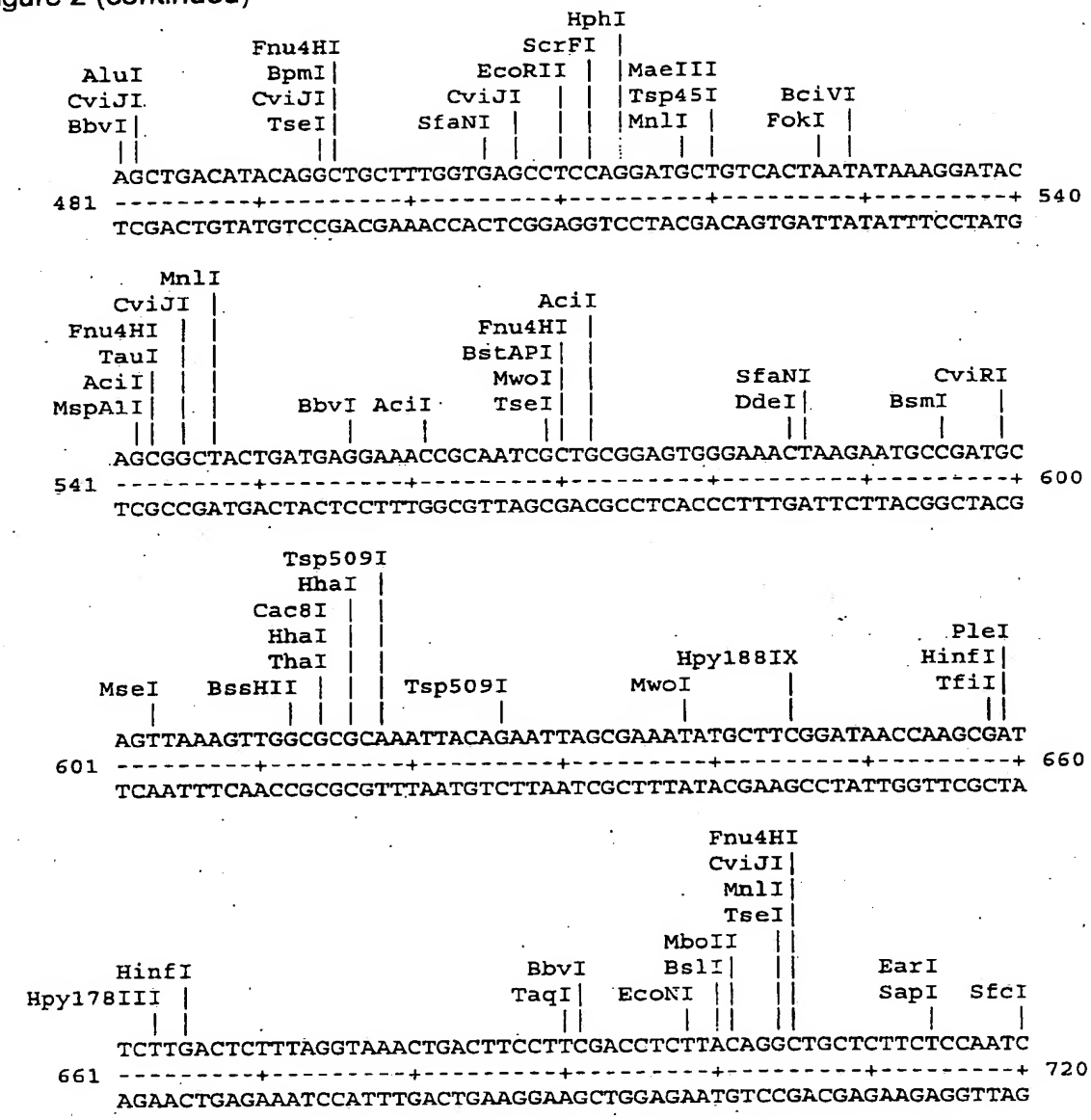


Figure 2 (continued)



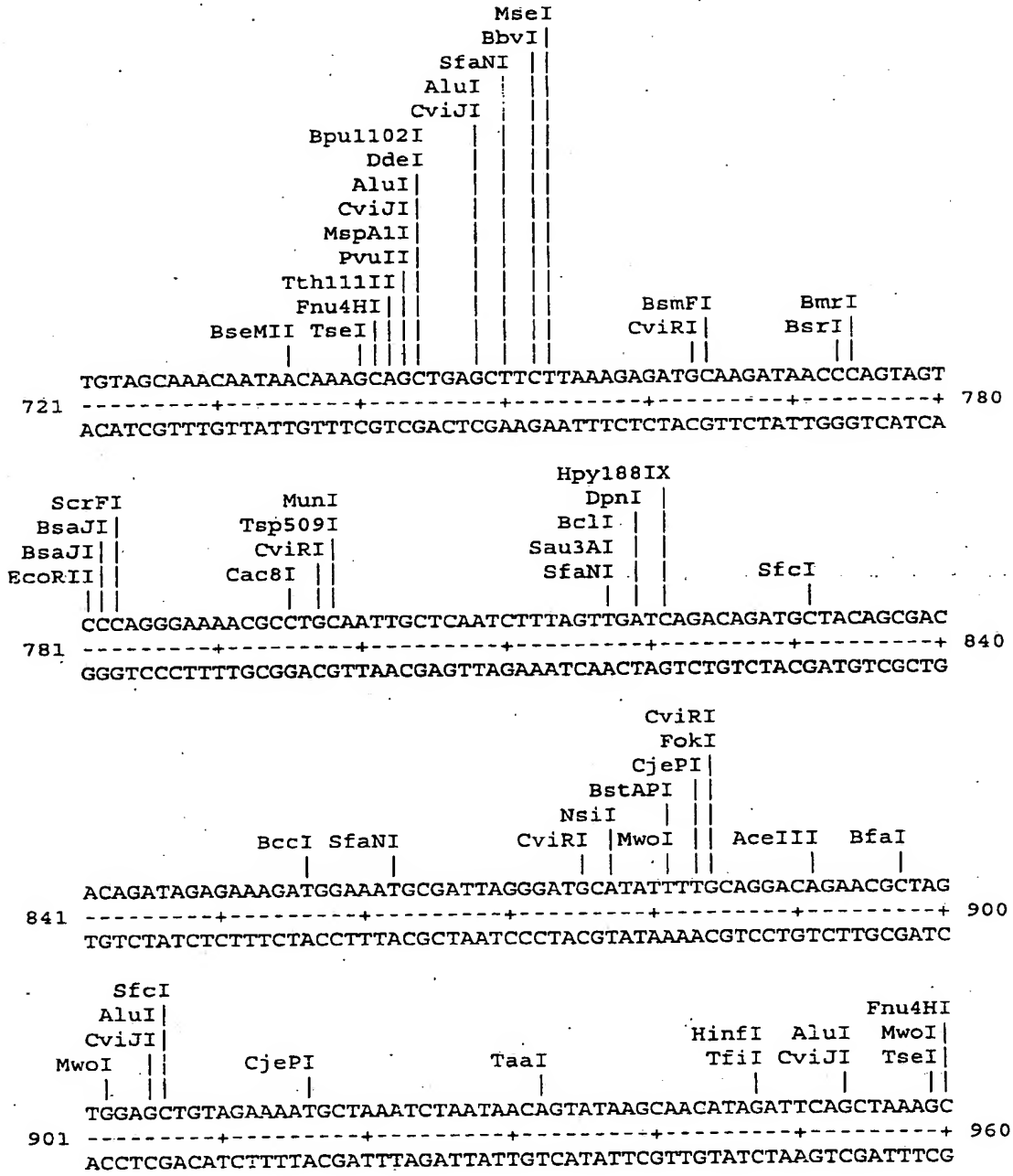
10045/0 .1 2004

Figure 2 (continued)



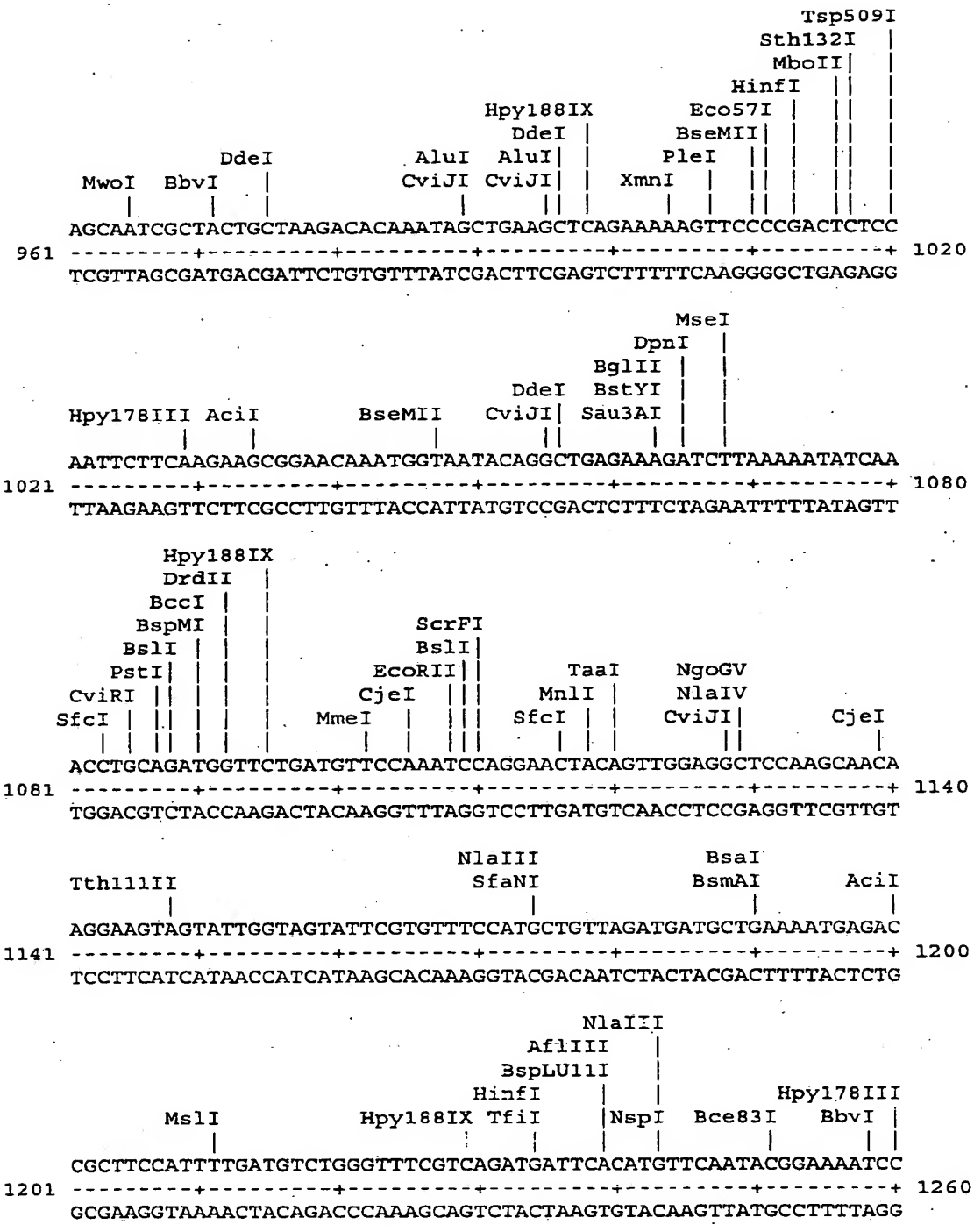
EP 1 247 871 A2 07-10-2002

Figure 2 (continued)



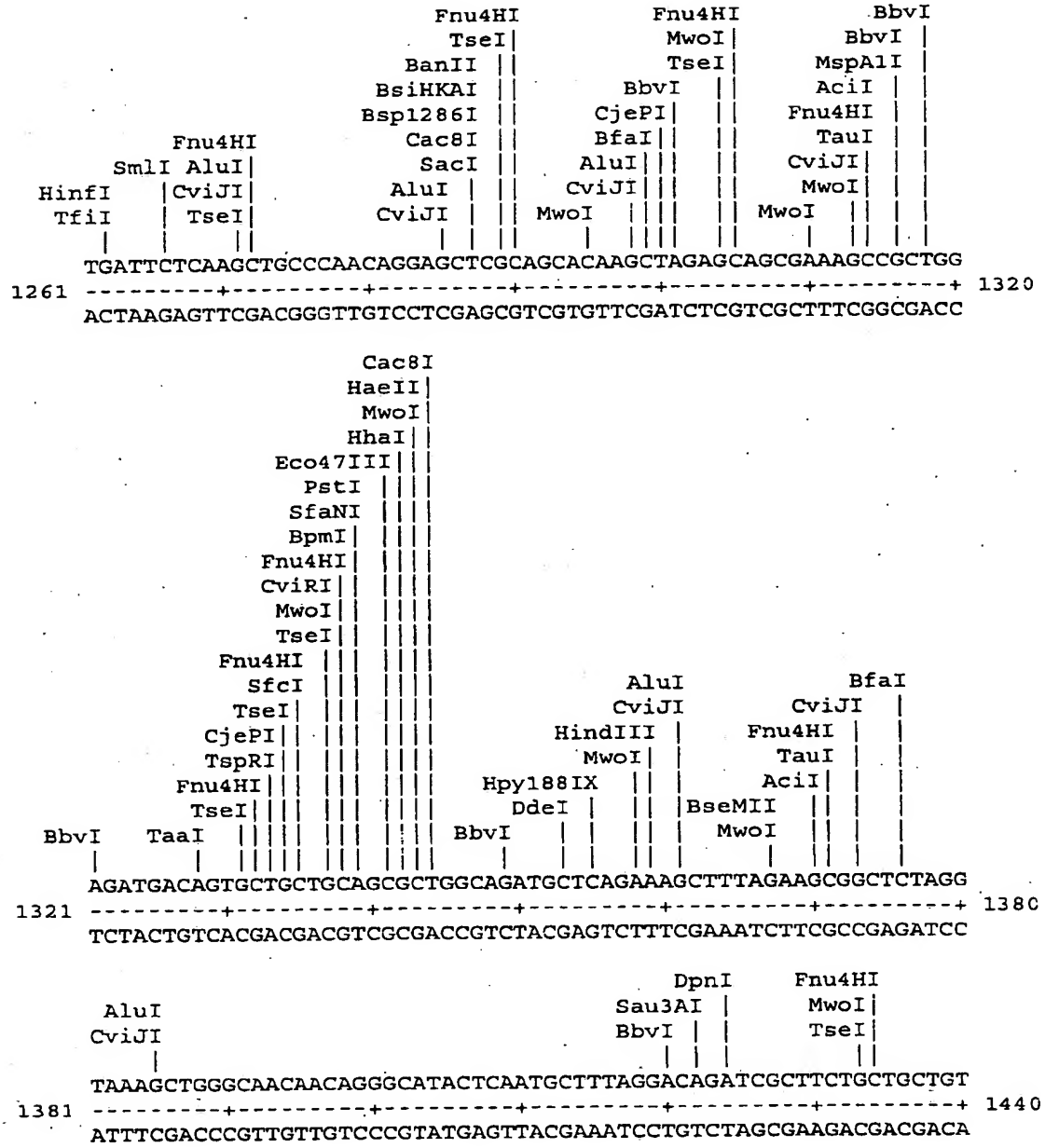
EP 0 746 614 B1

Figure 2 (continued)



Docket: 2945.1001

Figure 2 (continued)



WO 2004/076707 PCT/US2004/005474

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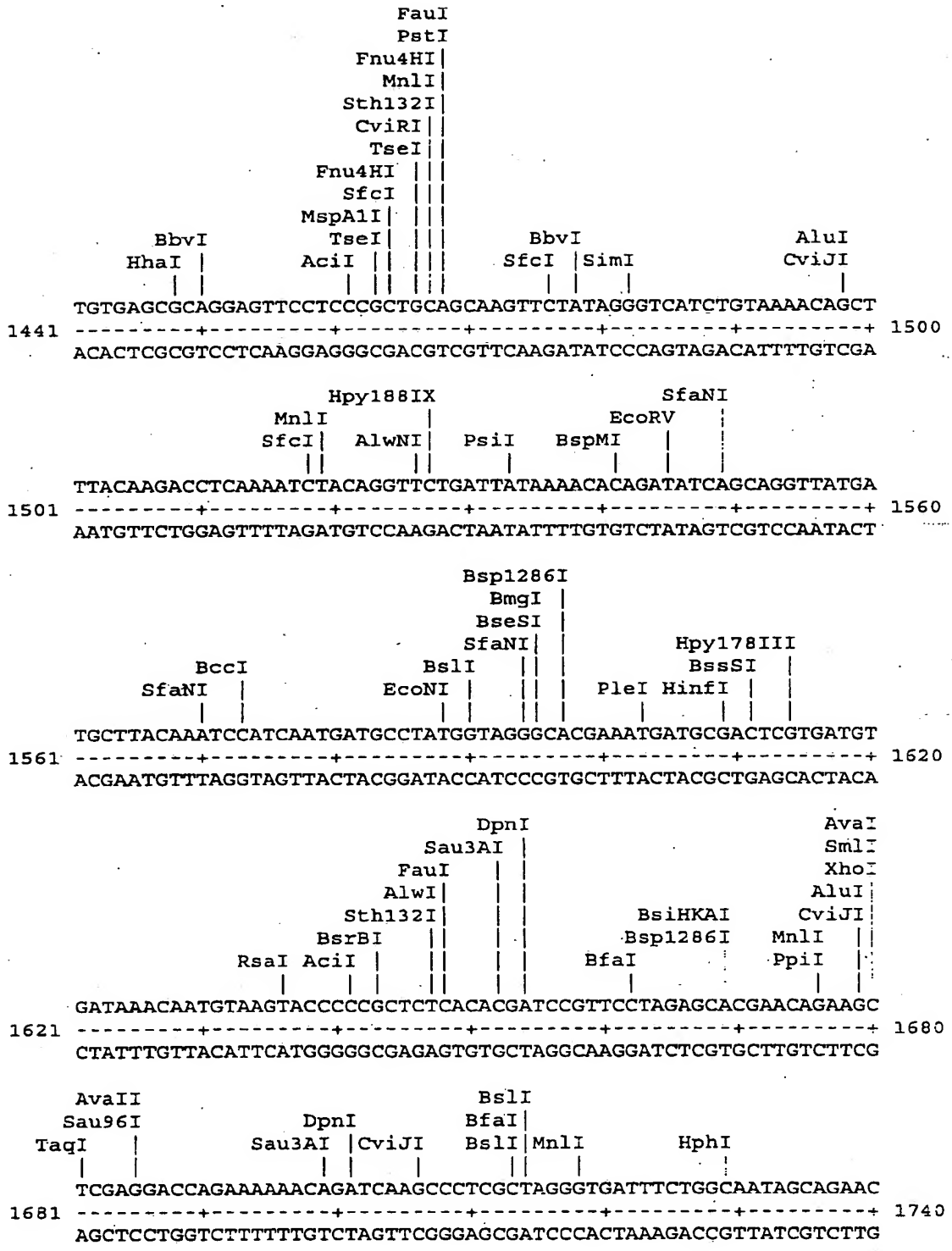

Figure 2 (continued)

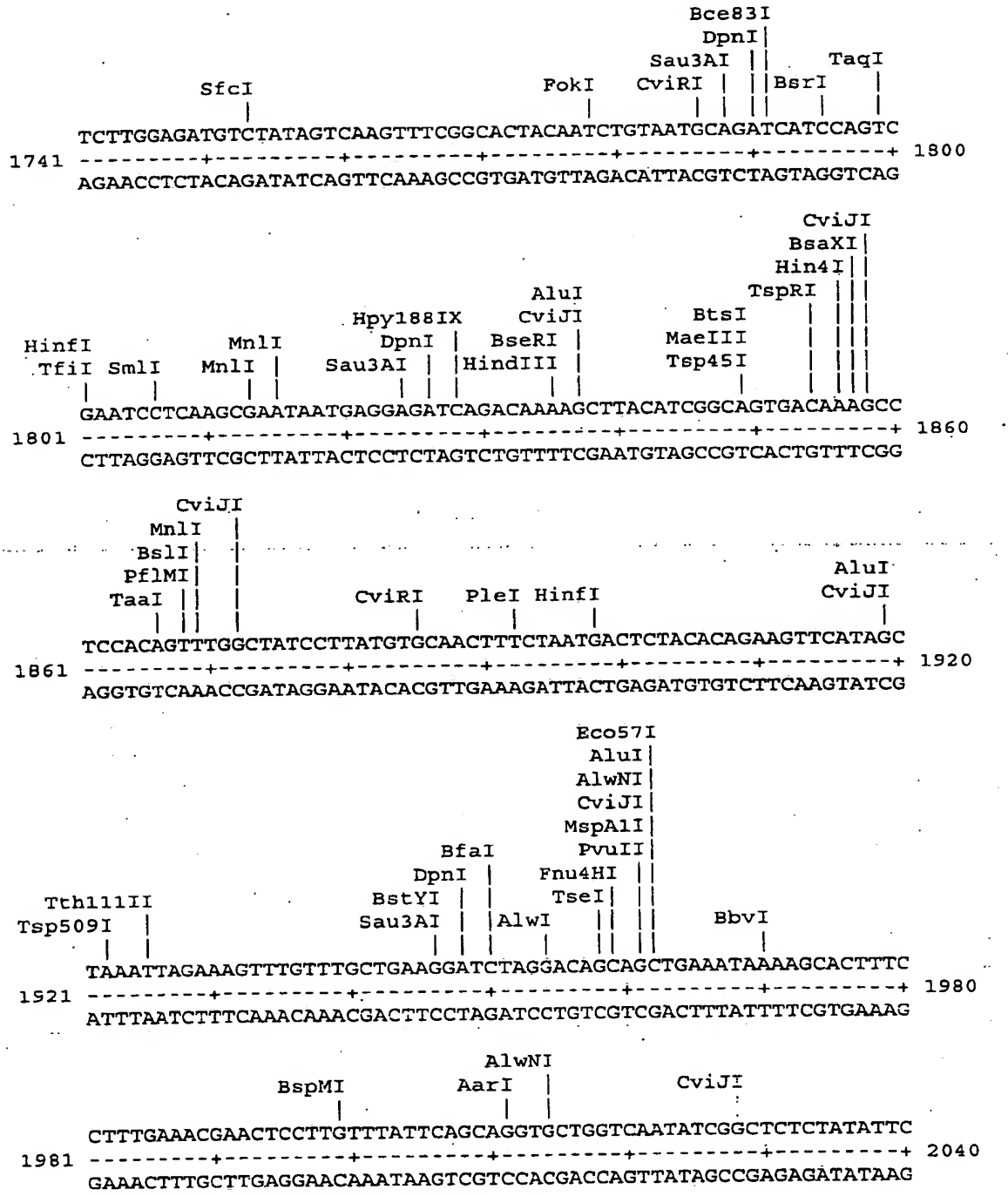

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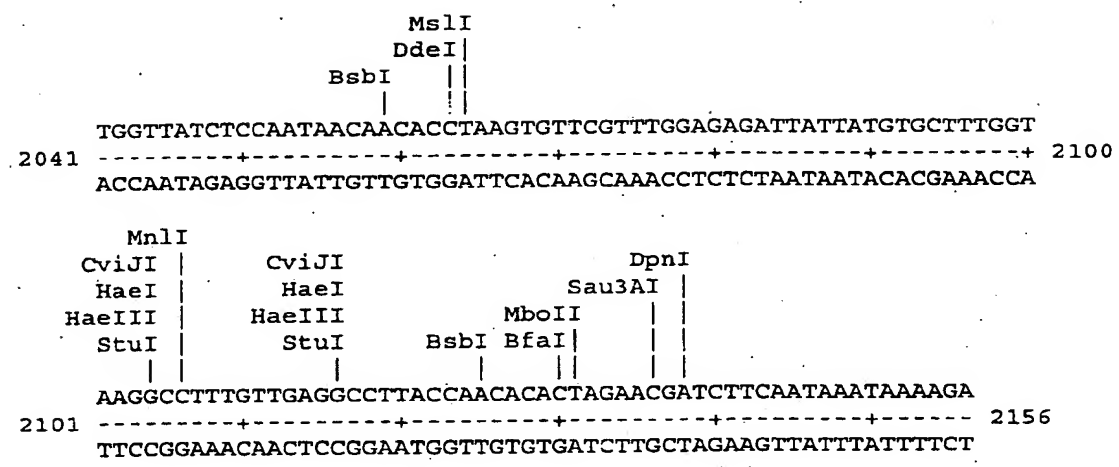
Figure 2 (continued)



1004467D 121401

Figure 3: Sequence Containing Truncated Version of *C. pneumoniae* 76kDa Gene; (nucleotides 1 to 665 and 2122 to 2238 are unrelated to the 76kDa Gene).

```
atgacaaaaa aacattatgc ttgggttgta gaagggattc tcaatcgttt gcctaaacag 60

ttttttgtga aatgtagtgt tgtcgactgg aacacattcg ttccttcaga aacctccact 120

acagaaaaag ctgctacaaa cgctatgaaa tacaaatact gtgtttggca gtggctcgtc 180

ggaaagcata gtcaggttcc ttggatcaat ggacagaaaa agcctctata tctttatgga 240

gctttcttaa tgaacccttt agcaaaggct acgaagacta cgttaaatgg aaaagaaaac 300

ctagcttggt ttattggagg aactttaggg ggactcagaa aagctggaga ctggtctgcc 360

acagtacgtt atgagtatgt cgaagccttg tcggttccag aaatagatgt ttcagggatt 420

ggccgtggta atttattaaa gttttggttc gcccaagcaa ttgctgctaa ctatgatcct 480

aaagaggcta atggttttac aaattataaa ggattttccg ctctatatat gtatggcatc 540

acagattctc tatcattcag agcttatggg gcttactcca aaccagcaaa cgataaactc 600

ggcagtgatt ttactttccg aaagtttgat ctaggtataa tttcagcgtt ttaagtcaaa 660

ttttaataaa atctttaaaa acaggctcgc attaattatt agtgagagct ttttttttat 720

tttttataat aaaactaaaa gatttttatt atttttgag ttttt atg gtt aat cct 777
                                              Met Val Asn Pro
                                                1

att ggt cca ggt cct ata gac gaa aca gaa cgc aca cct ccc gca gat 825
Ile Gly Pro Gly Pro Ile Asp Glu Thr Glu Arg Thr Pro Pro Ala Asp
  5                  10                  15                  20

ctt tct gct caa gga ttg gag gcg agt gca gca aat aag agt gcg gaa 873
Leu Ser Ala Gln Gly Leu Glu Ala Ser Ala Ala Asn Lys Ser Ala Glu
                25                  30                  35

gct caa aga ata gca ggt gcg gaa gct aag cct aaa gaa tct aag acc 921
Ala Gln Arg Ile Ala Gly Ala Glu Ala Lys Pro Lys Glu Ser Lys Thr
            40                  45                  50

gat tct gta gag cga tgg agc atc ttg cgt tct gca gtg aat gct ctc 969
Asp Ser Val Glu Arg Trp Ser Ile Leu Arg Ser Ala Val Asn Ala Leu
        55                  60                  65

atg agt ctg gca gat aag ctg ggt att gct tct agt aac agc tcg tct 1017
Met Ser Leu Ala Asp Lys Leu Gly Ile Ala Ser Ser Asn Ser Ser Ser
    70                  75                  80

tct act agc aga tct gca gac gtg gac tca acg aca gcg acc gca cct 1065
Ser Thr Ser Arg Ser Ala Asp Val Asp Ser Thr Thr Ala Thr Ala Pro
 85                  90                  95                  100
```

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Figure 3 (continued)

```
acg cct cct cca ccc acg ttt gat gat tat aag act caa gcg caa aca   1113
Thr Pro Pro Pro Pro Thr Phe Asp Asp Tyr Lys Thr Gln Ala Gln Thr
                105                 110                 115

gct tac gat act atc ttt acc tca aca tca cta gct gac ata cag gct   1161
Ala Tyr Asp Thr Ile Phe Thr Ser Thr Ser Leu Ala Asp Ile Gln Ala
            120                 125                 130

gct ttg gtg agc ctc cag gat gct gtc act aat ata aag gat aca gcg   1209
Ala Leu Val Ser Leu Gln Asp Ala Val Thr Asn Ile Lys Asp Thr Ala
        135                 140                 145

gct act gat gag gaa acc gca atc gct gcg gag tgg gaa act aag aat   1257
Ala Thr Asp Glu Glu Thr Ala Ile Ala Ala Glu Trp Glu Thr Lys Asn
    150                 155                 160

gcc gat gca gtt aaa gtt ggc gcg caa att aca gaa tta gcg aaa tat   1305
Ala Asp Ala Val Lys Val Gly Ala Gln Ile Thr Glu Leu Ala Lys Tyr
165                 170                 175                 180

gct tcg gat aac caa gcg att ctt gac tct tta ggt aaa ctg act tcc   1353
Ala Ser Asp Asn Gln Ala Ile Leu Asp Ser Leu Gly Lys Leu Thr Ser
                185                 190                 195

ttc gac ctc tta cag gct gct ctt ctc caa tct gta gca aac aat aac   1401
Phe Asp Leu Leu Gln Ala Ala Leu Leu Gln Ser Val Ala Asn Asn Asn
            200                 205                 210

aaa gca gct gag ctt ctt aaa gag atg caa gat aac cca gta gtc cca   1449
Lys Ala Ala Glu Leu Leu Lys Glu Met Gln Asp Asn Pro Val Val Pro
        215                 220                 225

ggg aaa acg cct gca att gct caa tct tta gtt gat cag aca gat gct   1497
Gly Lys Thr Pro Ala Ile Ala Gln Ser Leu Val Asp Gln Thr Asp Ala
    230                 235                 240

aca gcg aca cag ata gag aaa gat gga aat gcg att agg gat gca tat   1545
Thr Ala Thr Gln Ile Glu Lys Asp Gly Asn Ala Ile Arg Asp Ala Tyr
245                 250                 255                 260

ttt gca gga cag aac gct agt gga gct gta gaa aat gct aaa tct aat   1593
Phe Ala Gly Gln Asn Ala Ser Gly Ala Val Glu Asn Ala Lys Ser Asn
                265                 270                 275

aac agt ata agc aac ata gat tca gct aaa gca gca atc gct act gct   1641
Asn Ser Ile Ser Asn Ile Asp Ser Ala Lys Ala Ala Ile Ala Thr Ala
            280                 285                 290

aag aca caa ata gct gaa gct cag aaa aag ttc ccc gac tct cca att   1689
Lys Thr Gln Ile Ala Glu Ala Gln Lys Lys Phe Pro Asp Ser Pro Ile
        295                 300                 305
```

EP0947201A1

Figure 3 (continued)

```
ctt caa gaa gcg gaa caa atg gta ata cag gct gag aaa gat ctt aaa   1737
Leu Gln Glu Ala Glu Gln Met Val Ile Gln Ala Glu Lys Asp Leu Lys
    310                 315                 320

aat atc aaa cct gca gat ggt tct gat gtt cca aat cca gga act aca   1785
Asn Ile Lys Pro Ala Asp Gly Ser Asp Val Pro Asn Pro Gly Thr Thr
325                 330                 335                 340

gtt gga ggc tcc aag caa caa gga agt agt att ggt agt att cgt gtt   1833
Val Gly Gly Ser Lys Gln Gln Gly Ser Ser Ile Gly Ser Ile Arg Val
                345                 350                 355

tcc atg ctg tta gat gat gct gaa aat gag acc gct tcc att ttg atg   1881
Ser Met Leu Leu Asp Asp Ala Glu Asn Glu Thr Ala Ser Ile Leu Met
            360                 365                 370

tct ggg ttt cgt cag atg att cac atg ttc aat acg gaa aat cct gat   1929
Ser Gly Phe Arg Gln Met Ile His Met Phe Asn Thr Glu Asn Pro Asp
        375                 380                 385

tct caa gct gcc caa cag gag ctc gca gca caa gct aga gca gcg aaa   1977
Ser Gln Ala Ala Gln Gln Glu Leu Ala Ala Gln Ala Arg Ala Ala Lys
    390                 395                 400

gcc gct gga gat gac agt gct gct gca gcg ctg gca gat gct cag aaa   2025
Ala Ala Gly Asp Asp Ser Ala Ala Ala Ala Leu Ala Asp Ala Gln Lys
405                 410                 415                 420

gct tta gaa gcg gct cta ggt aaa gct ggg caa caa cag ggc ata ctc   2073
Ala Leu Glu Ala Ala Leu Gly Lys Ala Gly Gln Gln Gln Gly Ile Leu
                425                 430                 435

aat gct tta gga cag atc gct tct gct gct gtt gtg agc gca gga gta   2121
Asn Ala Leu Gly Gln Ile Ala Ser Ala Ala Val Val Ser Ala Gly Val
            440                 445                 450

ctc ccg ctg cag caa gtt cta tgg atc cga gct cgg tac caa gct tac   2169
Leu Pro Leu Gln Gln Val Leu Trp Ile Arg Ala Arg Tyr Gln Ala Tyr
        455                 460                 465

gta gaa caa aaa ctc atc tca gaa gag gat ctg aat agc gcc gtc gac   2217
Val Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Ser Ala Val Asp
    470                 475                 480

cat cat cat cat cat cat tga                                      2238
His His His His His His
485                 490
```

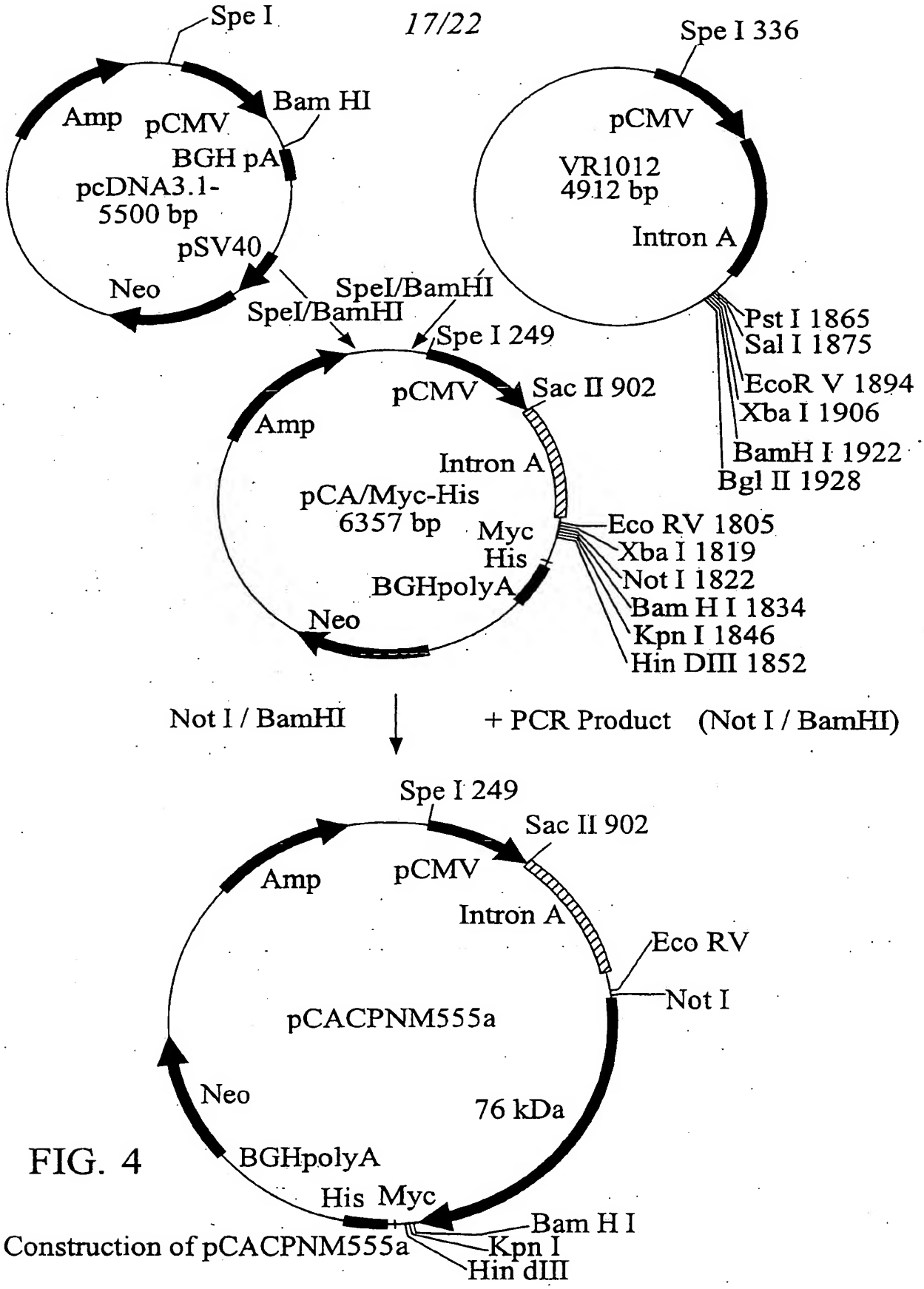

FIG. 4

Construction of pCACPNM555a

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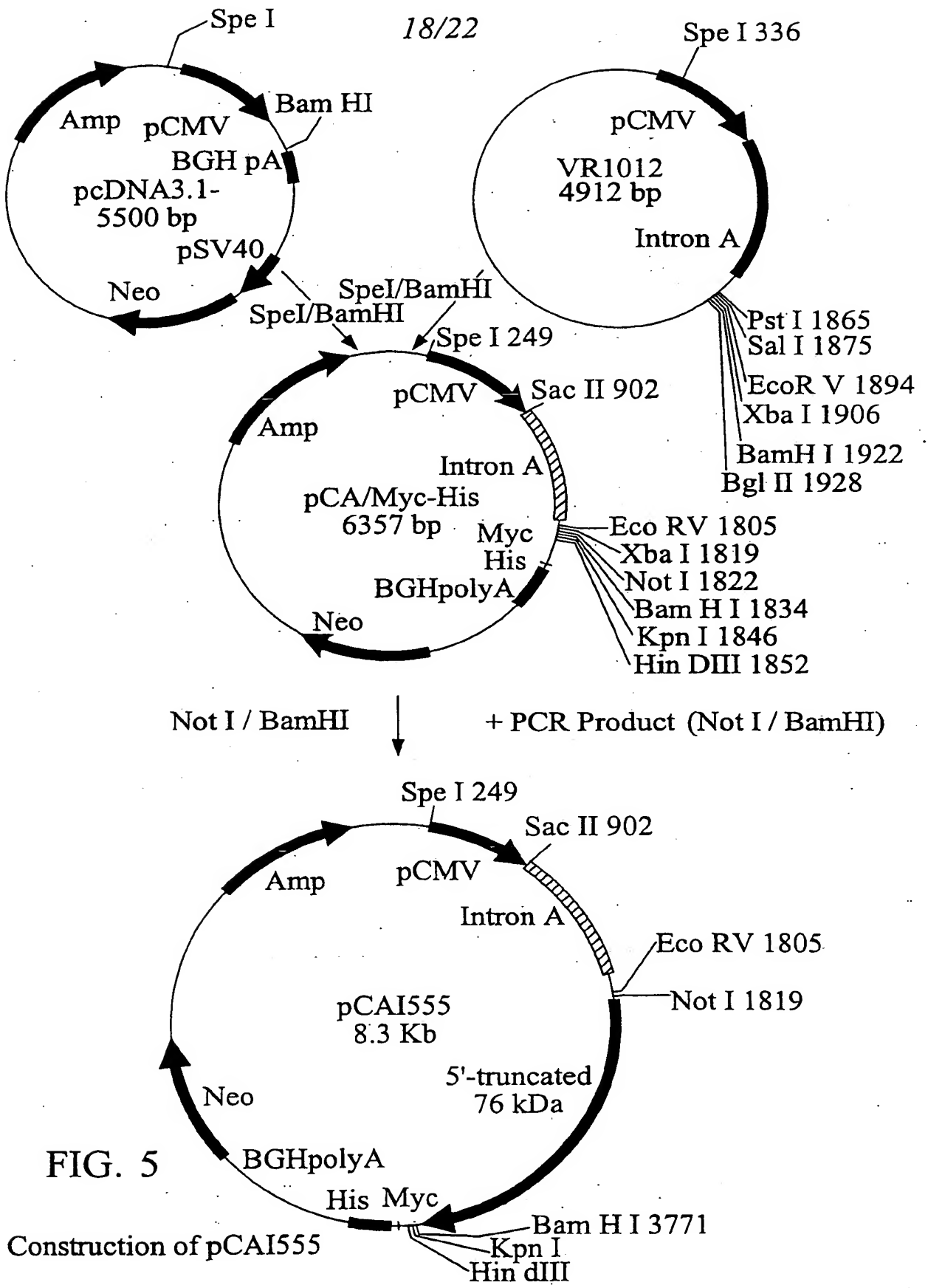


FIG. 5

Construction of pCAI555

EOHEZ4P5'0.1ZHP03

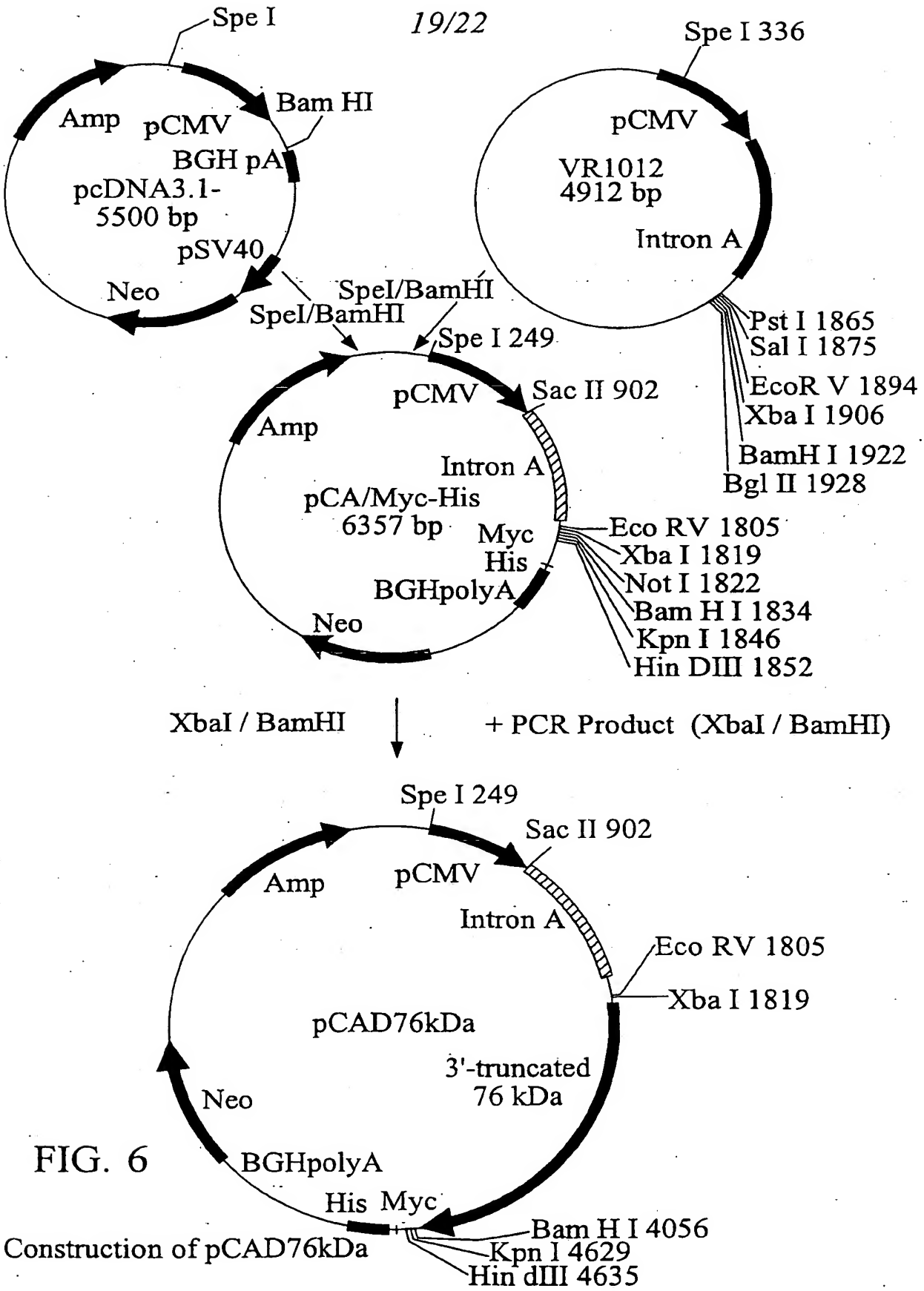


FIG. 6

Construction of pCAD76kDa

Exhibit 2154

Figure 7: pCACPNM555a Confers Protection Against *C. pneumoniae* Infection .

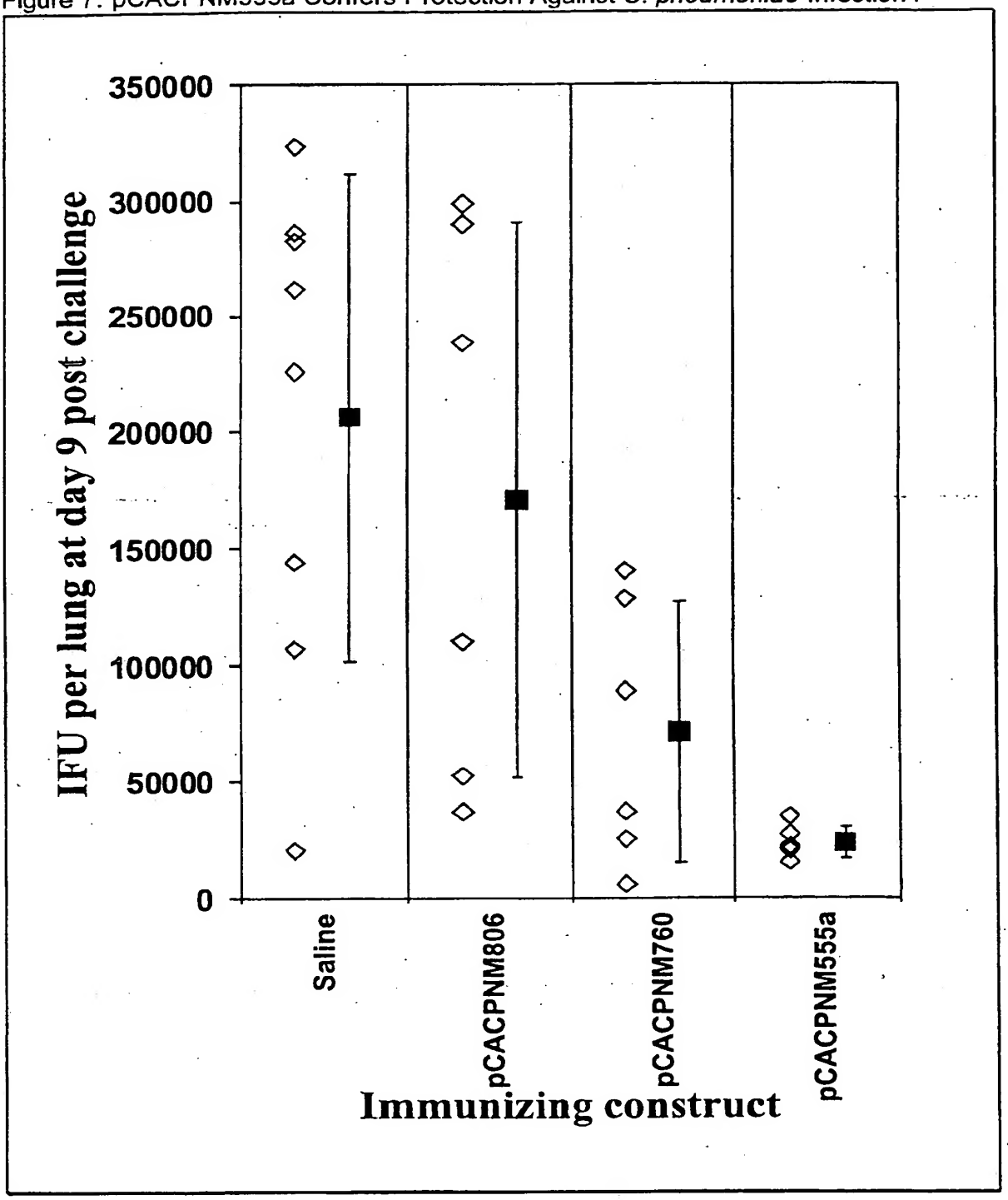


Figure 8: pCAI555 Confers Protection Against *C. pneumoniae* Infection.

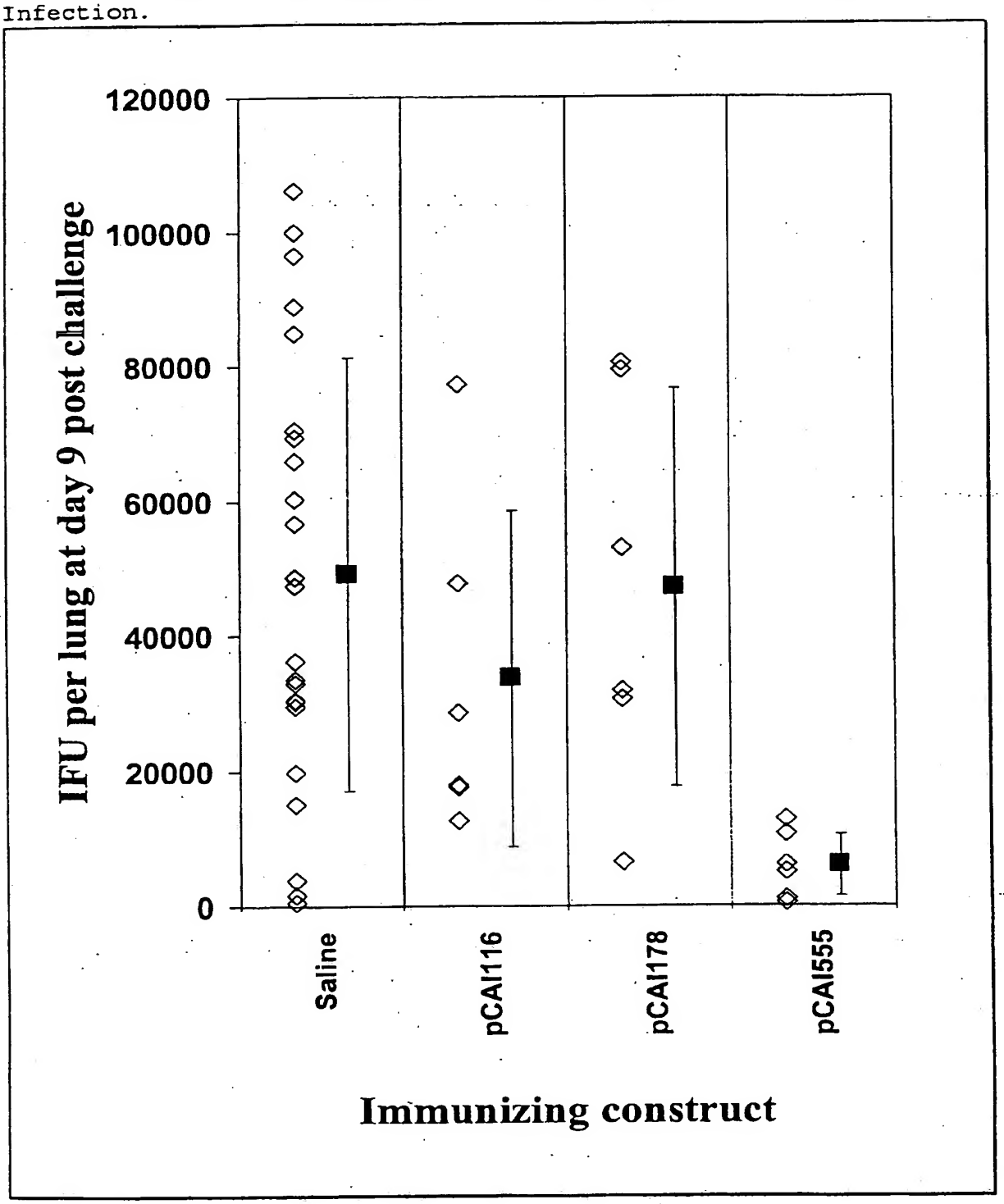
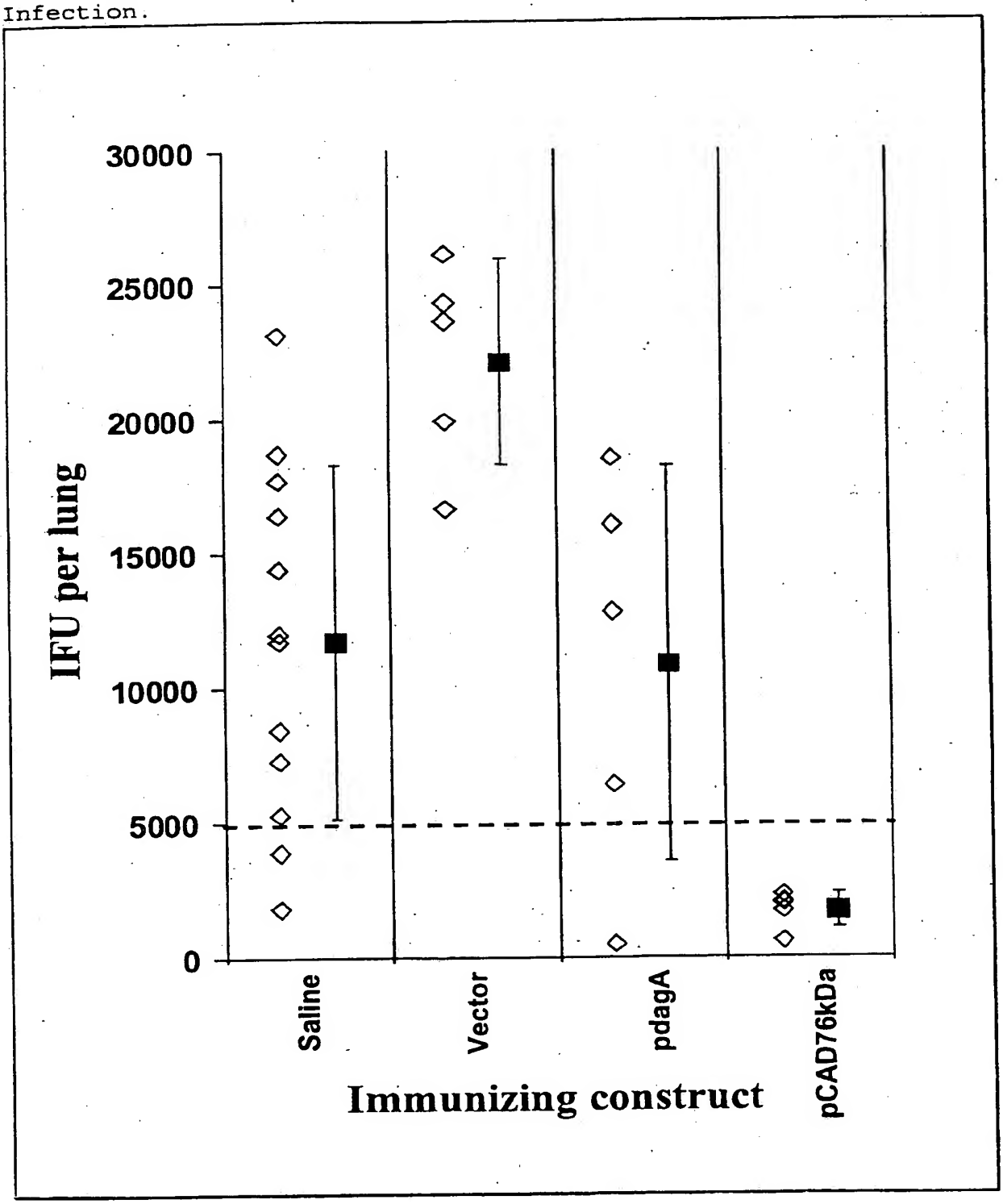


Figure 9: pCAD76kDa Confers Protection against *C. pneumoniae* Infection.



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